

SEQUENCE LISTING

<110> Rohm and Haas Company
Palli, Subba Reddy
Kapitskaya, Marianna Zinovjevna
Cress, Dean Ervin

<120> Novel Ecdysone Receptor-Based Inducible Gene Expression System

<130> A01020B

<140> Not Yet Assigned
<141> 2001-09-26

<150> 60/191,355
<151> 2000-03-22

<150> 60/269,799
<151> 2001-02-20

<150> PCT/US01/09050
<151> 2001-03-21

<160> 75

<170> PatentIn version 3.1

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caaatgttct cgatgaaggt ggacaacgtc gaatacgcgc ttctcactgc cattgtgatc 720
 ttctcggacc ggccgggcct ggagaaggcc caactagtcg aagcgatcca gagctactac 780
 atcgacacgc tacgcattta tataactcaac cgccactgcg gcgactcaat gagcctcgtc 840
 ttctacgcaa agctgctctc gatcctcacc gagctgcgta cgctgggcaa ccagaacgcc 900
 gagatgtggt tctcactaaa gctcaaaaac cgcaaactgc ccaagttcct cgaggagatc 960
 tgggacggt 969

<210> 11
 <211> 412
 <212> PRT
 <213> Choristoneura fumiferana

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 11

Lys Gly Pro Ala Pro Arg Gln Gln Glu Glu Leu Cys Leu Val Cys Gly
 1 5 10 15

Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu Gly Cys
 20 25 30

Lys Gly Phe Phe Arg Arg Ser Val Thr Lys Asn Ala Val Tyr Ile Cys
 35 40 45

Lys Phe Gly His Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys Cys
 50 55 60

Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro Glu
 65 70 75 80

Cys Val Val Pro Glu Thr Gln Cys Ala Met Lys Arg Lys Glu Lys Lys
 85 90 95

Ala Gln Lys Glu Lys Asp Lys Leu Pro Val Ser Thr Thr Thr Val Asp
 100 105 110

Asp His Met Pro Pro Ile Met Gln Cys Glu Pro Pro Pro Pro Glu Ala
 115 120 125

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Ala Arg Ile His Glu Val Val Pro Arg Phe Leu Ser Asp Lys Leu Leu
130 135 140

Glu Thr Asn Arg Gln Lys Asn Ile Pro Gln Leu Thr Ala Asn Gln Gln
145 150 155 160

Phe Leu Ile Ala Arg Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln Pro
165 170 175

Ser Asp Glu Asp Leu Lys Arg Ile Thr Gln Thr Trp Gln Gln Ala Asp
180 185 190

Asp Glu Asn Glu Glu Ser Asp Thr Pro Phe Arg Gln Ile Thr Glu Met
195 200 205

Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro
210 215 220

Gly Phe Ala Lys Ile Ser Gln Pro Asp Gln Ile Thr Leu Leu Lys Ala
225 230 235 240

Cys Ser Ser Glu Val Met Met Leu Arg Val Ala Arg Arg Tyr Asp Ala
245 250 255

Ala Ser Asp Ser Val Leu Phe Ala Asn Asn Gln Ala Tyr Thr Arg Asp
260 265 270

Asn Tyr Arg Lys Ala Gly Met Ala Tyr Val Ile Glu Asp Leu Leu His
275 280 285

Phe Cys Arg Cys Met Tyr Ser Met Ala Leu Asp Asn Ile His Tyr Ala
290 295 300

Leu Leu Thr Ala Val Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Gln
305 310 315 320

Pro Gln Leu Val Glu Glu Ile Gln Arg Tyr Tyr Leu Asn Thr Leu Arg
325 330 335

Ile Tyr Ile Leu Asn Gln Leu Ser Gly Ser Ala Arg Ser Ser Val Ile
340 345 350

Tyr Gly Lys Ile Leu Ser Ile Leu Ser Glu Leu Arg Thr Leu Gly Met

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355

360

365

Gln Asn Ser Asn Met Cys Ile Ser Leu Lys Leu Lys Asn Arg Lys Leu
370 375 380

Pro Pro Phe Leu Glu Glu Ile Trp Asp Val Ala Asp Met Ser His Thr
385 390 395 400

Gln Pro Pro Pro Ile Leu Glu Ser Pro Thr Asn Leu
405 410

<210> 12

<211> 412

<212> PRT

<213> Choristoneura fumiferana

<220>

<221> misc_feature

<223> Novel Sequence

<400> 12

Lys Gly Pro Ala Pro Arg Gln Gln Glu Glu Leu Cys Leu Val Cys Gly
1 5 10 15

Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu Gly Cys
20 25 30

Lys Gly Phe Phe Arg Arg Ser Val Thr Lys Asn Ala Val Tyr Ile Cys
35 40 45

Lys Phe Gly His Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys Cys
50 55 60

Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro Glu
65 70 75 80

Cys Val Val Pro Glu Thr Gln Cys Ala Met Lys Arg Lys Glu Lys Lys
85 90 95

Ala Gln Lys Glu Lys Asp Lys Leu Pro Val Ser Thr Thr Thr Val Asp
100 105 110

Asp His Met Pro Pro Ile Met Gln Cys Glu Pro Pro Pro Pro Glu Ala
115 120 125

Ala Arg Ile His Glu Val Val Pro Arg Phe Leu Ser Asp Lys Leu Leu
130 135 140

Glu Thr Asn Arg Gln Lys Asn Ile Pro Gln Leu Thr Ala Asn Gln Gln
145 150 155 160

Phe Leu Ile Ala Arg Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln Pro
165 170 175

Ser Asp Glu Asp Leu Lys Arg Ile Thr Gln Thr Trp Gln Gln Ala Asp
180 185 190

Asp Glu Asn Glu Glu Ser Asp Thr Pro Phe Arg Gln Ile Thr Glu Met
195 200 205

Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro
210 215 220

Gly Phe Ala Lys Ile Ser Gln Pro Asp Gln Ile Thr Leu Leu Lys Ala
225 230 235 240

Cys Ser Ser Glu Val Met Met Leu Arg Val Ala Arg Arg Tyr Asp Ala
245 250 255

Ala Ser Asp Ser Val Leu Phe Ala Asn Asn Gln Ala Tyr Thr Arg Asp
260 265 270

Asn Tyr Arg Lys Ala Gly Met Ala Tyr Val Ile Glu Asp Leu Leu His
275 280 285

Phe Cys Arg Cys Met Tyr Ser Met Ala Leu Asp Asn Ile His Tyr Ala
290 295 300

Leu Leu Thr Ala Val Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Gln
305 310 315 320

Pro Gln Leu Val Glu Glu Ile Gln Arg Tyr Tyr Leu Asn Thr Leu Arg
325 330 335

Ile Tyr Ile Leu Asn Gln Leu Ser Gly Ser Ala Arg Ser Ser Val Ile
340 345 350

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Tyr Gly Lys Ile Leu Ser Ile Leu Ser Glu Leu Arg Thr Leu Gly Met
 355 360 365

Gln Asn Ser Asn Met Cys Ile Ser Leu Lys Leu Lys Asn Arg Lys Leu
 370 375 380

Pro Pro Phe Leu Glu Glu Ile Trp Asp Val Ala Asp Met Ser His Thr
 385 390 395 400

Gln Pro Pro Pro Ile Leu Glu Ser Pro Thr Asn Leu
 405 410

<210> 13
 <211> 334
 <212> PRT
 <213> Choristoneura fumiferana

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 13

Pro Glu Cys Val Val Pro Glu Thr Gln Cys Ala Met Lys Arg Lys Glu
 1 5 10 15

Lys Lys Ala Gln Lys Glu Lys Asp Lys Leu Pro Val Ser Thr Thr Thr
 20 25 30

Val Asp Asp His Met Pro Pro Ile Met Gln Cys Glu Pro Pro Pro Pro
 35 40 45

Glu Ala Ala Arg Ile His Glu Val Val Pro Arg Phe Leu Ser Asp Lys
 50 55 60

Leu Leu Glu Thr Asn Arg Gln Lys Asn Ile Pro Gln Leu Thr Ala Asn
 65 70 75 80

Gln Gln Phe Leu Ile Ala Arg Leu Ile Trp Tyr Gln Asp Gly Tyr Glu
 85 90 95

Gln Pro Ser Asp Glu Asp Leu Lys Arg Ile Thr Gln Thr Trp Gln Gln
 100 105 110

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Ala Asp Asp Glu Asn Glu Glu Ser Asp Thr Pro Phe Arg Gln Ile Thr
115 120 125

Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly
130 135 140

Leu Pro Gly Phe Ala Lys Ile Ser Gln Pro Asp Gln Ile Thr Leu Leu
145 150 155 160

Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Val Ala Arg Arg Tyr
165 170 175

Asp Ala Ala Ser Asp Ser Val Leu Phe Ala Asn Asn Gln Ala Tyr Thr
180 185 190

Arg Asp Asn Tyr Arg Lys Ala Gly Met Ala Tyr Val Ile Glu Asp Leu
195 200 205

Leu His Phe Cys Arg Cys Met Tyr Ser Met Ala Leu Asp Asn Ile His
210 215 220

Tyr Ala Leu Leu Thr Ala Val Val Ile Phe Ser Asp Arg Pro Gly Leu
225 230 235 240

Glu Gln Pro Gln Leu Val Glu Glu Ile Gln Arg Tyr Tyr Leu Asn Thr
245 250 255

Leu Arg Ile Tyr Ile Leu Asn Gln Leu Ser Gly Ser Ala Arg Ser Ser
260 265 270

Val Ile Tyr Gly Lys Ile Leu Ser Ile Leu Ser Glu Leu Arg Thr Leu
275 280 285

Gly Met Gln Asn Ser Asn Met Cys Ile Ser Leu Lys Leu Lys Asn Arg
290 295 300

Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp Val Ala Asp Met Ser
305 310 315 320

His Thr Gln Pro Pro Pro Ile Leu Glu Ser Pro Thr Asn Leu
325 330

<211> 244
<212> PRT
<213> Choristoneura fumiferana

<220>
<221> misc_feature
<223> Novel Sequence

<400> 14

Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Asp Glu Asp Leu Lys Arg Ile
1 5 10 15

Thr Gln Thr Trp Gln Gln Ala Asp Asp Glu Asn Glu Glu Ser Asp Thr
20 25 30

Pro Phe Arg Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile
35 40 45

Val Glu Phe Ala Lys Gly Leu Pro Gly Phe Ala Lys Ile Ser Gln Pro
50 55 60

Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu
65 70 75 80

Arg Val Ala Arg Arg Tyr Asp Ala Ala Ser Asp Ser Val Leu Phe Ala
85 90 95

Asn Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ala
100 105 110

Tyr Val Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met
115 120 125

Ala Leu Asp Asn Ile His Tyr Ala Leu Leu Thr Ala Val Val Ile Phe
130 135 140

Ser Asp Arg Pro Gly Leu Glu Gln Pro Gln Leu Val Glu Glu Ile Gln
145 150 155 160

Arg Tyr Tyr Leu Asn Thr Leu Arg Ile Tyr Ile Leu Asn Gln Leu Ser
165 170 175

Gly Ser Ala Arg Ser Ser Val Ile Tyr Gly Lys Ile Leu Ser Ile Leu
180 185 190

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Ser Glu Leu Arg Thr Leu Gly Met Gln Asn Ser Asn Met Cys Ile Ser
 195 200 205

Leu Lys Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp
 210 215 220

Asp Val Ala Asp Met Ser His Thr Gln Pro Pro Pro Ile Leu Glu Ser
 225 230 235 240

Pro Thr Asn Leu

<210> 15
 <211> 320
 <212> PRT
 <213> Choristoneura fumiferana

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 15

Pro Glu Cys Val Val Pro Glu Thr Gln Cys Ala Met Lys Arg Lys Glu
 1 5 10 15

Lys Lys Ala Gln Lys Glu Lys Asp Lys Leu Pro Val Ser Thr Thr Thr
 20 25 30

Val Asp Asp His Met Pro Pro Ile Met Gln Cys Glu Pro Pro Pro Pro
 35 40 45

Glu Ala Ala Arg Ile His Glu Val Val Pro Arg Phe Leu Ser Asp Lys
 50 55 60

Leu Leu Glu Thr Asn Arg Gln Lys Asn Ile Pro Gln Leu Thr Ala Asn
 65 70 75 80

Gln Gln Phe Leu Ile Ala Arg Leu Ile Trp Tyr Gln Asp Gly Tyr Glu
 85 90 95

Gln Pro Ser Asp Glu Asp Leu Lys Arg Ile Thr Gln Thr Trp Gln Gln
 100 105 110

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Ala Asp Asp Glu Asn Glu Glu Ser Asp Thr Pro Phe Arg Gln Ile Thr
 115 120 125

Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly
 130 135 140

Leu Pro Gly Phe Ala Lys Ile Ser Gln Pro Asp Gln Ile Thr Leu Leu
 145 150 155 160

Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Val Ala Arg Arg Tyr
 165 170 175

Asp Ala Ala Ser Asp Ser Val Leu Phe Ala Asn Asn Gln Ala Tyr Thr
 180 185 190

Arg Asp Asn Tyr Arg Lys Ala Gly Met Ala Tyr Val Ile Glu Asp Leu
 195 200 205

Leu His Phe Cys Arg Cys Met Tyr Ser Met Ala Leu Asp Asn Ile His
 210 215 220

Tyr Ala Leu Leu Thr Ala Val Val Ile Phe Ser Asp Arg Pro Gly Leu
 225 230 235 240

Glu Gln Pro Gln Leu Val Glu Glu Ile Gln Arg Tyr Tyr Leu Asn Thr
 245 250 255

Leu Arg Ile Tyr Ile Leu Asn Gln Leu Ser Gly Ser Ala Arg Ser Ser
 260 265 270

Val Ile Tyr Gly Lys Ile Leu Ser Ile Leu Ser Glu Leu Arg Thr Leu
 275 280 285

Gly Met Gln Asn Ser Asn Met Cys Ile Ser Leu Lys Leu Lys Asn Arg
 290 295 300

Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp Val Ala Asp Met Ser
 305 310 315 320

<210> 16

<211> 625

<212> PRT

<213> Drosophila melanogaster

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<220>
<221> misc_feature
<223> Novel Sequence

<400> 16

Gly Pro Ala Pro Arg Val Gln Glu Glu Leu Cys Leu Val Cys Gly Asp
1 5 10 15

Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu Gly Cys Lys
20 25 30

Gly Phe Phe Arg Arg Ser Val Thr Lys Ser Ala Val Tyr Cys Cys Lys
35 40 45

Phe Gly Arg Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys Cys Gln
50 55 60

Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro Glu Cys
65 70 75 80

Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys Lys Ala
85 90 95

Gln Lys Glu Lys Asp Lys Met Thr Thr Ser Pro Ser Ser Gln His Gly
100 105 110

Gly Asn Gly Ser Leu Ala Ser Gly Gly Gly Gln Asp Phe Val Lys Lys
115 120 125

Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro Gln His Ala Thr Ile
130 135 140

Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys Cys Gln Ala Arg Asn Ile
145 150 155 160

Pro Ser Leu Thr Tyr Asn Gln Leu Ala Val Ile Tyr Lys Leu Ile Trp
165 170 175

Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Arg Arg Ile
180 185 190

Met Ser Gln Pro Asp Glu Asn Glu Ser Gln Thr Asp Val Ser Phe Arg

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195

200

205

His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe
 210 215 220

Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp Gln Ile
 225 230 235 240

Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Met Ala
 245 250 255

Arg Arg Tyr Asp His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg
 260 265 270

Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile
 275 280 285

Glu Asp Leu Leu His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp
 290 295 300

Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg
 305 310 315 320

Pro Gly Leu Glu Lys Ala Gln Leu Val Glu Ala Ile Gln Ser Tyr Tyr
 325 330 335

Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His Cys Gly Asp Ser
 340 345 350

Met Ser Leu Val Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu
 355 360 365

Arg Thr Leu Gly Asn Gln Asn Ala Glu Met Cys Phe Ser Leu Lys Leu
 370 375 380

Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val His
 385 390 395 400

Ala Ile Pro Pro Ser Val Gln Ser His Leu Gln Ile Thr Gln Glu Glu
 405 410 415

Asn Glu Arg Leu Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly
 420 425 430

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Ala Ile Thr Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala
 435 440 445

Ala Ala Ala Ala Gln His Gln Pro Gln Pro Gln Pro Gln Pro Gln Pro
 450 455 460

Ser Ser Leu Thr Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu
 465 470 475 480

Gln Pro Gln Leu Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu
 485 490 495

Gln Pro Gln Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro
 500 505 510

Gln Leu Leu Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro
 515 520 525

Gly Ser Leu Ser Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser
 530 535 540

Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala
 545 550 555 560

Ala Val Thr Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly
 565 570 575

Val Gly Val Gly Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn
 580 585 590

Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln
 595 600 605

Glu Gln Leu Ile Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr
 610 615 620

Ala
 625

<210> 17
 <211> 583
 <212> PRT

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<213> Drosophila melanogaster

<220>

<221> misc_feature

<223> Novel Sequence

<400> 17

Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met Asp Met Tyr
1 5 10 15

Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val
20 25 30

Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys Ala Met Lys
35 40 45

Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met Thr Thr Ser
50 55 60

Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser Gly Gly Gly
65 70 75 80

Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr Cys Glu Pro
85 90 95

Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys
100 105 110

Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln Leu Ala Val
115 120 125

Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu
130 135 140

Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn Glu Ser Gln
145 150 155 160

Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile Leu Thr Val
165 170 175

Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile
180 185 190

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Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val
 195 200 205

Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser Asp Ser Ile
 210 215 220

Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala
 225 230 235 240

Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys Arg Gln Met
 245 250 255

Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile
 260 265 270

Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln Leu Val Glu
 275 280 285

Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn
 290 295 300

Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala Lys Leu Leu
 305 310 315 320

Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn Ala Glu Met
 325 330 335

Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu
 340 345 350

Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln Ser His Leu
 355 360 365

Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala Glu Arg Met
 370 375 380

Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp Cys Asp Ser
 385 390 395 400

Ala Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln Pro Gln Pro
 405 410 415

Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp Ser Gln His

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420

425

430

Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln Leu Gln Gly
435 440 445

Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln Leu Gln Pro
450 455 460

Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala Pro Val Pro
465 470 475 480

Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser Thr Ser Ser
485 490 495

Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr
500 505 510

Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr Thr Ser Ala
515 520 525

Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val Gly Gly Asn
530 535 540

Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu Met Gly Val
545 550 555 560

Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val Ala Val Lys
565 570 575

Ser Glu His Ser Thr Thr Ala
580

<210> 18
<211> 549
<212> PRT
<213> Drosophila melanogaster

<220>
<221> misc_feature
<223> Novel Sequence

<400> 18

Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg
1 5 10 15

Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met Thr Thr Ser Pro Ser
 20 25 30

Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser Gly Gly Gly Gln Asp
 35 40 45

Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro Gln
 50 55 60

His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys Cys Gln
 65 70 75 80

Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln Leu Ala Val Ile Tyr
 85 90 95

Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp
 100 105 110

Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn Glu Ser Gln Thr Asp
 115 120 125

Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu
 130 135 140

Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln
 145 150 155 160

Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met
 165 170 175

Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser Asp Ser Ile Phe Phe
 180 185 190

Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met
 195 200 205

Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys Arg Gln Met Phe Ser
 210 215 220

Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile
 225 230 235 240

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Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln Leu Val Glu Ala Ile
245 250 255

Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His
260 265 270

Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala Lys Leu Leu Ser Ile
275 280 285

Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn Ala Glu Met Cys Phe
290 295 300

Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile
305 310 315 320

Trp Asp Val His Ala Ile Pro Pro Ser Val Gln Ser His Leu Gln Ile
325 330 335

Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala Glu Arg Met Arg Ala
340 345 350

Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp Cys Asp Ser Ala Ser
355 360 365

Thr Ser Ala Ala Ala Ala Ala Ala Gln His Gln Pro Gln Pro Gln Pro
370 375 380

Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp Ser Gln His Gln Thr
385 390 395 400

Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln Leu Gln Gly Gln Leu
405 410 415

Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln Leu Gln Pro Gln Ile
420 425 430

Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala Pro Val Pro Ala Ser
435 440 445

Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser Thr Ser Ser Glu Tyr
450 455 460

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Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr Thr Ser
465 470 475 480

Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr Thr Ser Ala Val Pro
485 490 495

Met Gly Asn Gly Val Gly Val Gly Val Gly Gly Asn Val Ser
500 505 510

Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala Leu
515 520 525

His Ser His Gln Glu Gln Leu Ile Gly Gly Val Ala Val Lys Ser Glu
530 535 540

His Ser Thr Thr Ala
545

<210> 19
<211> 445
<212> PRT
<213> Drosophila melanogaster

<220>
<221> misc_feature
<223> Novel Sequence

<400> 19

Tyr Glu Gln Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro
1 5 10 15

Asp Glu Asn Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu
20 25 30

Ile Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu
35 40 45

Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys
50 55 60

Ala Cys Ser Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp
65 70 75 80

His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg

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85

90

95

Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu
 100 105 110

His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr
 115 120 125

Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu
 130 135 140

Lys Ala Gln Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu
 145 150 155 160

Arg Ile Tyr Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val
 165 170 175

Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly
 180 185 190

Asn Gln Asn Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys
 195 200 205

Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro
 210 215 220

Ser Val Gln Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu
 225 230 235 240

Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala
 245 250 255

Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Ala
 260 265 270

Gln His Gln Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr
 275 280 285

Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu
 290 295 300

Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu
 305 310 315 320

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Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro
 325 330 335

Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser
 340 345 350

Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly
 355 360 365

Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala
 370 375 380

Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly
 385 390 395 400

Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala
 405 410 415

Met Ala Leu Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile
 420 425 430

Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr Ala
 435 440 445

<210> 20
 <211> 323
 <212> PRT
 <213> Drosophila melanogaster

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 20

Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg
 1 5 10 15

Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met Thr Thr Ser Pro Ser
 20 25 30

Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser Gly Gly Gly Gln Asp
 35 40 45

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Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro Gln
50 55 60

His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys Cys Gln
65 70 75 80

Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln Leu Ala Val Ile Tyr
85 90 95

Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp
100 105 110

Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn Glu Ser Gln Thr Asp
115 120 125

Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu
130 135 140

Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln
145 150 155 160

Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met
165 170 175

Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser Asp Ser Ile Phe Phe
180 185 190

Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met
195 200 205

Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys Arg Gln Met Phe Ser
210 215 220

Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile
225 230 235 240

Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln Leu Val Glu Ala Ile
245 250 255

Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His
260 265 270

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Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala Lys Leu Leu Ser Ile
 275 280 285

Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn Ala Glu Met Cys Phe
 290 295 300

Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile
 305 310 315 320

Trp Asp Val

<210> 21
 <211> 987
 <212> DNA
 <213> Mus musculus
 <220>
 <221> misc_feature
 <223> Novel Sequence

<400> 21
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 tgcaagggct tcttcaagag gacagtagcg aaagacctga cctacacctg ccgagacaac 120
 aaggactgcc tgatcgacaa gagacagcgg aaccgggtgtc agtactgccg ctaccagaag 180
 tgcttgccca tgggcatgaa gcgggaagct gtgcaggagg agcggcagcg gggcaaggac 240
 cggaatgaga acgaggtgga gtccaccagc agtgccaacg aggacatgcc tntagagaag 300
 attctggaag ccgagcttgc tgtcgagccc aagactgaga catacgtgga ggcaaactg 360
 gggctgaacc ccagctcacc aaatgaccct gttaccaaca tctgtcaagc agcagacaag 420
 cagctcttca ctcttggtga gtgggccaag aggatccac acttttctga gctgccctta 480
 gacgaccagg tcctctgct acgggcaggc tggaaacgagc tgctgatcgc ctcttctcc 540
 caccgtcca tagctgtgaa agatgggatt ctcttgcca ccggcctgca cgtacaccgg 600
 aacagcgctc acagtgtggt ggtgggccc atctttgaca ggggtgtaac agagctgggtg 660
 tctaagatgc gtgacatgca gatggacaag acggagctgg gctgcctgcg agccattgtc 720
 ctgttcaacc ctgactctaa ggggctctca aacctgctg aggtggaggc gttgagggag 780
 aaggtgtatg cgtcactaga agcgtactgc aaacacaagt accctgagca gccgggcagg 840
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cacctgttct tcttcaagct catcggggac acgcccacg acaccttct catggagatg 960

ctggaggcac cacatcaagc cacctag 987

<210> 22

<211> 789

<212> DNA

<213> Mus musculus

<220>

<221> misc_feature

<223> Novel Sequence

<400> 22

aagcgggaag ctgtgcagga ggagcggcag cggggcaagg accggaatga gaacgaggtg 60

gagtcacca gcagtgccaa cgaggacatg cctgtagaga agattctgga agccgagctt 120

gctgtcgagc ccaagactga gacatactg gaggcaaaca tggggctgaa cccagctca 180

ccaaatgacc ctgttacc aa catctgtcaa gcagcagaca agcagctctt cactcttctg 240

gagtgggcca agaggatccc acacttttct gagctgcccc tagacgacca ggtcatcctg 300

ctacgggcag gctggaacga gctgctgac gcctccttct cccaccgctc catagctgtg 360

aaagatggga ttctcctggc caccggcctg cacgtacacc ggaacagcgc tcacagtgtc 420

ggggtgggcg ccatctttga cagggtgcta acagagctgg tgtctaagat gcgtgacatg 480

cagatggaca agacggagct gggctgcctg cgagccattg tctgttcaa cctgactct 540

aaggggctct caaacctgc tgaggtggag gcgttgaggg agaaggtgta tgcgtcacta 600

gaagcgtact gcaaacacaa gtaccctgag cagccgggca ggtttgccaa gctgctgctc 660

cgctgcctg cactgcgttc catcgggctc aagtgcctgg agcacctgtt cttcttcaag 720

ctcatcgggg acacgcccac cgacaccttc ctcatggaga tgctggaggc accacatcaa 780

gccacctag 789

<210> 23

<211> 714

<212> DNA

<213> Mus musculus

<220>

<221> misc_feature

<223> Novel Sequence

<400> 23

gccaacgagg acatgcctgt agagaagatt ctggaagccg agcttgctgt cgagcccaag 60

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actgagacat acgtggaggg aaacatgggg ctgaaccca gctcaccaa tgaccctgtt 120
 accaacaatct gtcaagcagc agacaagcag ctcttcactc ttgtggagtg ggccaagagg 180
 atccccacact tttctgagct gcccttagac gaccagggtca tcctgctacg ggcaggctgg 240
 aacgagctgc tgatcgctc cttctccac cgctccatag ctgtgaaaga tgggattctc 300
 ctggccaccg gcctgcacgt acaccggaac agcgctcaca gtgctggggg gggcgccatc 360
 tttgacaggg tgctaacaga gctggtgtct aagatgcgtg acatgcagat ggacaagacg 420
 gagctggggt gcctgcgagc cattgtcctg ttcaaccctg actctaaggg gctctcaaac 480
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 cacaagtacc ctgagcagcc gggcagggtt gccaaagtgc tgctccgcct gcctgcactg 600
 cgttccatcg ggctcaagtg cctggagcac ctgttcttct tcaagctcat cggggacacg 660
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<210> 24
 <211> 536
 <212> DNA
 <213> Mus musculus
 <220>
 <221> misc_feature
 <223> Novel Sequence

<400> 24
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 tcctggccac cggcctgcac gtacaccgga acagcgctca cagtgtggg gtgggcgcca 180
 tctttgacag ggtgctaaca gagctggtgt ctaagatgctg tgacatgcag atggacaaga 240
 cggagctggg ctgcctgcga gccattgtcc tgttcaacc tgactctaag gggctctcaa 300
 accctgctga ggtggaggcg ttgagggaga aggtgtatgc gtcactagaa gcgtactgca 360
 aacacaagta ccctgagcag ccgggcagggt ttgccaagct gctgctccgc ctgcctgcac 420
 tgcgttccat cgggctcaag tgcttgagc acctgttctt cttcaagctc atcggggaca 480
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<210> 25
 <211> 672
 <212> DNA

<213> Mus musculus

<220>

<221> misc_feature

<223> Novel Sequence

<400> 25

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accaacatct gtcaagcagc agacaagcag ctcttcactc ttgtggagtg ggccaagagg 180
atcccacact tttctgagct gcccctagac gaccaggtca tcttgctacg ggagggctgg 240
aacgagctgc tgatcgctc cttctccac cgctccatag ctgtgaaaga tgggattctc 300
ctggccaccg gcctgcacgt acaccggaac agcgctcaca gtgctggggg gggcgccatc 360
tttgacaggg tgctaacaga gctgggtgtct aagatgcgtg acatgcagat ggacaagacg 420
gagctgggct gcctgcgagc cattgtcctg ttcaaccctg actctaaggg gctctcaaac 480
cctgctgagg tggaggcggt gagggagaag gtgtatgcgt cactagaagc gtactgcaaa 540
cacaagtacc ctgagcagcc gggcaggttt gccaaagctgc tgctccgcct gcctgcactg 600
cgttccatcg ggctcaagtg cctggagcac ctgttcttct tcaagctcat cggggacacg 660
cccatcgaca cc 672

<210> 26

<211> 1123

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Novel Sequence

<400> 26

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aaggactgcc tgattgacaa gcggcagcgg aaccggtgcc agtactgccg ctaccagaag 180
tgcttgcca tgggcatgaa gcgggaagcc gtgcaggagg agcggcagcg tggcaaggac 240
cggaacgaga atgaggtgga gtcgaccagc agcgccaacg aggacatgcc ggtggagagg 300
atcctggagg ctgagctggc cgtggagccc aagaccgaga cctacgtgga ggcaaactg 360
gggctgaacc ccagctcgcc gaacgacct gtcaccaaca ttgccaagc agccgacaaa 420

cagcttttca ccctggtgga gtgggccaag cggatcccac acttctcaga gctgccccctg 480
gacgaccagg tcattcctgct gcgggcaggc tggaatgagc tgctcatcgc ctcccttctcc 540
caccgctcca tcgccgtgaa ggacgggatc ctccctggcca cggggctgca cgtccaccgg 600
aacagcgccc acagcgcagg ggtggggcgcc atctttgaca ggggtgctgac ggagcttgtg 660
tccaagatgc gggacatgca gatggacaag acggagctgg gctgcctgcg cgccatcgtc 720
ctctttaacc ctgactccaa ggggctctcg aaccgggccc aggtggaggc gctgaggagg 780
aaggtctatg cgtccttggg ggcctactgc aagcacaagt acccagagca gccgggaagg 840
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ctggaggcgc cgcaccaa at gacttaggcc tcggggccca tcctttgtgc ccaccgttc 1020
tggccacct gcctggacgc cagctgttct tctcagcctg agccctgtcc ctgcccttct 1080
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<210> 27
<211> 925
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> Novel Sequence

<400> 27
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gccgtggagc ccaagaccga gacctacgtg gaggcaaaca tggggctgaa cccagctcg 180
ccgaacgacc ctgtcaccaa catttgccaa gcagccgaca aacagctttt caccctggtg 240
gagtgggcca agcggatccc acatttctca gagctgcccc tggacgacca ggtcatcctg 300
ctgcgggcag gctggaatga gctgctcatc gcctccttct ccaccgctc catcgccgtg 360
aaggacggga tcctcctggc caccgggctg cacgtccacc ggaacagcgc ccacagcgca 420
ggggtgggag ccatctttga cagggtgctg acggagcttg tgtccaagat gcgggacatg 480
cagatggaca agacggagct gggctgcctg cgcgccatcg tcctctttaa ccctgactcc 540
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gaggcctact gcaagcacia gtaccagag cagccgggaa ggctcgctaa gctcttgctc 660
cgctgcccgg ctctgcgctc catcgggctc aaatgcctgg aacatctctt cttcttcaag 720
ctcatcgggg acacacccat tgacaccttc cttatggaga tgctggaggc gccgcaccaa 780
atgacttagg cctgcggggc catcctttgt gcccaccctg tctggccacc ctgcctggac 840
gccagctgtt cttctcagcc tgagccctgt ccttgccctt ctctgcctgg cctgtttgga 900
ctttggggca cagcctgtca ctgct 925

<210> 28
<211> 850
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Novel Sequence

<400> 28
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accaacattt gccaagcagc cgacaaacag cttttcacc tgggtggagt ggccaagcgg 180
atcccacact tctcagagct gccctggac gaccaggtea tcttgctgcg ggcaggctgg 240
aatgagctgc tcatcgctc cttctccac cgctccatcg ccgtgaagga cgggatcctc 300
ctggccaccg ggctgcacgt ccaccggaac agcgcccaca gcgcaggggt gggcgccatc 360
tttgacaggg tgctgacgga gcttgtgtcc aagatgcggg acatgcagat ggacaagacg 420
gagctgggct gcctgcgcgc catcgctctc tttaacctg actccaaggg gctctcgaac 480
ccggccgagg tggaggcgct gagggagaag gtctatgcgt ccttggaggc ctactgcaag 540
cacaagtacc cagagcagcc gggaggttc gctaagctct tgctccgct gccggctctg 600
cgctccatcg ggctcaaatg cctggaacat ctcttcttct tcaagctcat cggggacaca 660
cccattgaca ccttcttat ggagatgctg gaggcgccgc accaaatgac ttaggcctgc 720
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tgtcactgct 850

<210> 29
<211> 670

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<212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <223> Novel Sequence

<400> 29
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 aatgagctgc tcatcgccctc cttctcccac cgctccatcg ccgtgaagga cgggatcctc 120
 ctggccaccg ggctgcacgt ccaccggaac agcgcccaca gcgcaggggt gggcgccatc 180
 tttgacaggg tgctgacgga gcttgtgtcc aagatgcggg acatgcagat ggacaagacg 240
 gagctgggct gcctgcgcgc catcgctctc tttaaccctg actccaaggg gctctcgaac 300
 ccggccgagg tggaggcgct gagggagaag gtctatgcgt ccttgagggc ctactgcaag 360
 cacaagtacc cagagcagcc gggaagggtc gctaagctct tgctccgcct gccggctctg 420
 cgctccatcg ggctcaaagt cctggaacat ctcttcttct tcaagctcat cggggacaca 480
 cccattgaca ccttccttat ggagatgctg gaggcgccgc accaaatgac ttaggcctgc 540
 gggcccatcc tttgtgcca cccgttctgg ccaccctgcc tggacgccag ctgttcttct 600
 cagcctgagc cctgtccctg cccttctctg cctggcctgt ttggactttg gggcacagcc 660
 tgtcactgct 670

<210> 30
 <211> 672
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <223> Novel Sequence

<400> 30
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 accgagacct acgtggaggc aaacatgggg ctgaaccca gctcgccgaa cgaccctgtc 120
 accaacattt gccaaagcagc cgacaaacag cttttcaccc tggaggagtg ggccaagcgg 180
 atccacact tctcagagct gcccctggac gaccaggtca tcctgctgcg ggcaggctgg 240
 aatgagctgc tcatcgccctc cttctcccac cgctccatcg ccgtgaagga cgggatcctc 300
 ctggccaccg ggctgcacgt ccaccggaac agcgcccaca gcgcaggggt gggcgccatc 360

tttgacaggg tgctgacgga gcttgtgtcc aagatgcggg acatgcagat ggacaagacg 420
gagctgggct gcctgcgcgc catcgtcctc ttttaaccctg actccaaggg gctctcgaac 480
ccggccgagg tggaggcgct gagggagaag gtctatgcgt ccttggaggc ctactgcaag 540
cacaagtacc cagagcagcc gggaagggtc gctaagctct tgctccgcct gccggctctg 600
cgctccatcg ggctcaaatz cctggaacat ctcttcttct tcaagctcat cggggacaca 660
cccattgaca cc 672

<210> 31
<211> 328
<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<223> Novel Sequence

<400> 31

Cys Ala Ile Cys Gly Asp Arg Ser Ser Gly Lys His Tyr Gly Val Tyr
1 5 10 15

Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asp
20 25 30

Leu Thr Tyr Thr Cys Arg Asp Asn Lys Asp Cys Leu Ile Asp Lys Arg
35 40 45

Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys Leu Ala Met
50 55 60

Gly Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Gly Lys Asp
65 70 75 80

Arg Asn Glu Asn Glu Val Glu Ser Thr Ser Ser Ala Asn Glu Asp Met
85 90 95

Pro Val Glu Lys Ile Leu Glu Ala Glu Leu Ala Val Glu Pro Lys Thr
100 105 110

Glu Thr Tyr Val Glu Ala Asn Met Gly Leu Asn Pro Ser Ser Pro Asn
115 120 125

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Asp Pro Val Thr Asn Ile Cys Gln Ala Ala Asp Lys Gln Leu Phe Thr
130 135 140

Leu Val Glu Trp Ala Lys Arg Ile Pro His Phe Ser Glu Leu Pro Leu
145 150 155 160

Asp Asp Gln Val Ile Leu Leu Arg Ala Gly Trp Asn Glu Leu Leu Ile
165 170 175

Ala Ser Phe Ser His Arg Ser Ile Ala Val Lys Asp Gly Ile Leu Leu
180 185 190

Ala Thr Gly Leu His Val His Arg Asn Ser Ala His Ser Ala Gly Val
195 200 205

Gly Ala Ile Phe Asp Arg Val Leu Thr Glu Leu Val Ser Lys Met Arg
210 215 220

Asp Met Gln Met Asp Lys Thr Glu Leu Gly Cys Leu Arg Ala Ile Val
225 230 235 240

Leu Phe Asn Pro Asp Ser Lys Gly Leu Ser Asn Pro Ala Glu Val Glu
245 250 255

Ala Leu Arg Glu Lys Val Tyr Ala Ser Leu Glu Ala Tyr Cys Lys His
260 265 270

Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu
275 280 285

Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe
290 295 300

Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp Thr Phe Leu Met Glu Met
305 310 315 320

Leu Glu Ala Pro His Gln Ala Thr
325

<210> 32

<211> 262

<212> PRT

<213> Mus musculus

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<220>
<221> misc_feature
<223> Novel Sequence

<400> 32

Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Gly Lys Asp Arg Asn
1 5 10 15

Glu Asn Glu Val Glu Ser Thr Ser Ser Ala Asn Glu Asp Met Pro Val
20 25 30

Glu Lys Ile Leu Glu Ala Glu Leu Ala Val Glu Pro Lys Thr Glu Thr
35 40 45

Tyr Val Glu Ala Asn Met Gly Leu Asn Pro Ser Ser Pro Asn Asp Pro
50 55 60

Val Thr Asn Ile Cys Gln Ala Ala Asp Lys Gln Leu Phe Thr Leu Val
65 70 75 80

Glu Trp Ala Lys Arg Ile Pro His Phe Ser Glu Leu Pro Leu Asp Asp
85 90 95

Gln Val Ile Leu Leu Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ser
100 105 110

Phe Ser His Arg Ser Ile Ala Val Lys Asp Gly Ile Leu Leu Ala Thr
115 120 125

Gly Leu His Val His Arg Asn Ser Ala His Ser Ala Gly Val Gly Ala
130 135 140

Ile Phe Asp Arg Val Leu Thr Glu Leu Val Ser Lys Met Arg Asp Met
145 150 155 160

Gln Met Asp Lys Thr Glu Leu Gly Cys Leu Arg Ala Ile Val Leu Phe
165 170 175

Asn Pro Asp Ser Lys Gly Leu Ser Asn Pro Ala Glu Val Glu Ala Leu
180 185 190

Arg Glu Lys Val Tyr Ala Ser Leu Glu Ala Tyr Cys Lys His Lys Tyr
195 200 205

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Pro Glu Gln Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ala
210 215 220

Leu Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe Phe Lys
225 230 235 240

Leu Ile Gly Asp Thr Pro Ile Asp Thr Phe Leu Met Glu Met Leu Glu
245 250 255

Ala Pro His Gln Ala Thr
260

<210> 33
<211> 237
<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<223> Novel Sequence

<400> 33

Ala Asn Glu Asp Met Pro Val Glu Lys Ile Leu Glu Ala Glu Leu Ala
1 5 10 15

Val Glu Pro Lys Thr Glu Thr Tyr Val Glu Ala Asn Met Gly Leu Asn
20 25 30

Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala Ala Asp
35 40 45

Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His Phe
50 55 60

Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala Gly Trp
65 70 75 80

Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Ala Val Lys
85 90 95

Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn Ser Ala
100 105 110

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His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr Glu Leu
115 120 125

Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr Glu Leu Gly Cys
130 135 140

Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys Gly Leu Ser Asn
145 150 155 160

Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr Ala Ser Leu Glu
165 170 175

Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala Lys
180 185 190

Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys Leu
195 200 205

Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp Thr
210 215 220

Phe Leu Met Glu Met Leu Glu Ala Pro His Gln Ala Thr
225 230 235

<210> 34
<211> 177
<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<223> Novel Sequence

<400> 34

Ile Pro His Phe Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu
1 5 10 15

Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser
20 25 30

Ile Ala Val Lys Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His
35 40 45

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Arg Asn Ser Ala His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val
50 55 60

Leu Thr Glu Leu Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr
65 70 75 80

Glu Leu Gly Cys Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys
85 90 95

Gly Leu Ser Asn Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr
100 105 110

Ala Ser Leu Glu Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly
115 120 125

Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly
130 135 140

Leu Lys Cys Leu Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr
145 150 155 160

Pro Ile Asp Thr Phe Leu Met Glu Met Leu Glu Ala Pro His Gln Ala
165 170 175

Thr

<210> 35
<211> 224
<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<223> Novel Sequence

<400> 35

Ala Asn Glu Asp Met Pro Val Glu Lys Ile Leu Glu Ala Glu Leu Ala
1 5 10 15

Val Glu Pro Lys Thr Glu Thr Tyr Val Glu Ala Asn Met Gly Leu Asn
20 25 30

Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala Ala Asp

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35

40

45

Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His Phe
 50 55 60

Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala Gly Trp
 65 70 75 80

Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Ala Val Lys
 85 90 95

Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn Ser Ala
 100 105 110

His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr Glu Leu
 115 120 125

Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr Glu Leu Gly Cys
 130 135 140

Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys Gly Leu Ser Asn
 145 150 155 160

Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr Ala Ser Leu Glu
 165 170 175

Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala Lys
 180 185 190

Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys Leu
 195 200 205

Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp Thr
 210 215 220

<210> 36

<211> 328

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Novel Sequence

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<400> 36

Cys Ala Ile Cys Gly Asp Arg Ser Ser Gly Lys His Tyr Gly Val Tyr
1 5 10 15

Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asp
20 25 30

Leu Thr Tyr Thr Cys Arg Asp Asn Lys Asp Cys Leu Ile Asp Lys Arg
35 40 45

Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys Leu Ala Met
50 55 60

Gly Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Gly Lys Asp
65 70 75 80

Arg Asn Glu Asn Glu Val Glu Ser Thr Ser Ser Ala Asn Glu Asp Met
85 90 95

Pro Val Glu Arg Ile Leu Glu Ala Glu Leu Ala Val Glu Pro Lys Thr
100 105 110

Glu Thr Tyr Val Glu Ala Asn Met Gly Leu Asn Pro Ser Ser Pro Asn
115 120 125

Asp Pro Val Thr Asn Ile Cys Gln Ala Ala Asp Lys Gln Leu Phe Thr
130 135 140

Leu Val Glu Trp Ala Lys Arg Ile Pro His Phe Ser Glu Leu Pro Leu
145 150 155 160

Asp Asp Gln Val Ile Leu Leu Arg Ala Gly Trp Asn Glu Leu Leu Ile
165 170 175

Ala Ser Phe Ser His Arg Ser Ile Ala Val Lys Asp Gly Ile Leu Leu
180 185 190

Ala Thr Gly Leu His Val His Arg Asn Ser Ala His Ser Ala Gly Val
195 200 205

Gly Ala Ile Phe Asp Arg Val Leu Thr Glu Leu Val Ser Lys Met Arg
210 215 220

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Asp Met Gln Met Asp Lys Thr Glu Leu Gly Cys Leu Arg Ala Ile Val
225 230 235 240

Leu Phe Asn Pro Asp Ser Lys Gly Leu Ser Asn Pro Ala Glu Val Glu
245 250 255

Ala Leu Arg Glu Lys Val Tyr Ala Ser Leu Glu Ala Tyr Cys Lys His
260 265 270

Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu
275 280 285

Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe
290 295 300

Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp Thr Phe Leu Met Glu Met
305 310 315 320

Leu Glu Ala Pro His Gln Met Thr
325

<210> 37
<211> 262
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Novel Sequence

<400> 37

Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Gly Lys Asp Arg Asn
1 5 10 15

Glu Asn Glu Val Glu Ser Thr Ser Ser Ala Asn Glu Asp Met Pro Val
20 25 30

Glu Arg Ile Leu Glu Ala Glu Leu Ala Val Glu Pro Lys Thr Glu Thr
35 40 45

Tyr Val Glu Ala Asn Met Gly Leu Asn Pro Ser Ser Pro Asn Asp Pro
50 55 60

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Val Thr Asn Ile Cys Gln Ala Ala Asp Lys Gln Leu Phe Thr Leu Val
65 70 75 80

Glu Trp Ala Lys Arg Ile Pro His Phe Ser Glu Leu Pro Leu Asp Asp
85 90 95

Gln Val Ile Leu Leu Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ser
100 105 110

Phe Ser His Arg Ser Ile Ala Val Lys Asp Gly Ile Leu Leu Ala Thr
115 120 125

Gly Leu His Val His Arg Asn Ser Ala His Ser Ala Gly Val Gly Ala
130 135 140

Ile Phe Asp Arg Val Leu Thr Glu Leu Val Ser Lys Met Arg Asp Met
145 150 155 160

Gln Met Asp Lys Thr Glu Leu Gly Cys Leu Arg Ala Ile Val Leu Phe
165 170 175

Asn Pro Asp Ser Lys Gly Leu Ser Asn Pro Ala Glu Val Glu Ala Leu
180 185 190

Arg Glu Lys Val Tyr Ala Ser Leu Glu Ala Tyr Cys Lys His Lys Tyr
195 200 205

Pro Glu Gln Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ala
210 215 220

Leu Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe Phe Lys
225 230 235 240

Leu Ile Gly Asp Thr Pro Ile Asp Thr Phe Leu Met Glu Met Leu Glu
245 250 255

Ala Pro His Gln Met Thr
260

<210> 38
<211> 237
<212> PRT
<213> Homo sapiens

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<220>
<221> misc_feature
<223> Novel Sequence

<400> 38

Ala Asn Glu Asp Met Pro Val Glu Arg Ile Leu Glu Ala Glu Leu Ala
1 5 10 15

Val Glu Pro Lys Thr Glu Thr Tyr Val Glu Ala Asn Met Gly Leu Asn
20 25 30

Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala Ala Asp
35 40 45

Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His Phe
50 55 60

Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala Gly Trp
65 70 75 80

Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Ala Val Lys
85 90 95

Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn Ser Ala
100 105 110

His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr Glu Leu
115 120 125

Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr Glu Leu Gly Cys
130 135 140

Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys Gly Leu Ser Asn
145 150 155 160

Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr Ala Ser Leu Glu
165 170 175

Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala Lys
180 185 190

Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys Leu
195 200 205

0956703-037601

Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp Thr
 210 215 220

Phe Leu Met Glu Met Leu Glu Ala Pro His Gln Met Thr
 225 230 235

<210> 39
 <211> 177
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 39

Ile Pro His Phe Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu
 1 5 10 15

Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser
 20 25 30

Ile Ala Val Lys Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His
 35 40 45

Arg Asn Ser Ala His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val
 50 55 60

Leu Thr Glu Leu Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr
 65 70 75 80

Glu Leu Gly Cys Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys
 85 90 95

Gly Leu Ser Asn Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr
 100 105 110

Ala Ser Leu Glu Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly
 115 120 125

Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly
 130 135 140

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Leu Lys Cys Leu Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr
145 150 155 160

Pro Ile Asp Thr Phe Leu Met Glu Met Leu Glu Ala Pro His Gln Met
165 170 175

Thr

<210> 40
<211> 224
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Novel Sequence

<400> 40

Ala Asn Glu Asp Met Pro Val Glu Arg Ile Leu Glu Ala Glu Leu Ala
1 5 10 15

Val Glu Pro Lys Thr Glu Thr Tyr Val Glu Ala Asn Met Gly Leu Asn
20 25 30

Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala Ala Asp
35 40 45

Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His Phe
50 55 60

Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala Gly Trp
65 70 75 80

Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Ala Val Lys
85 90 95

Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn Ser Ala
100 105 110

His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr Glu Leu
115 120 125

09965703-092601

Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr Glu Leu Gly Cys
130 135 140

Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys Gly Leu Ser Asn
145 150 155 160

Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr Ala Ser Leu Glu
165 170 175

Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala Lys
180 185 190

Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys Leu
195 200 205

Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp Thr
210 215 220

<210> 41
<211> 198
<212> DNA
<213> Choristoneura fumiferana

<400> 41
tgtctggtat gcggggacag agcctccgga taccactaca atgcgctcac gtgtgaaggg 60
tgtaaagggt tcttcagacg gagtgttacc aaaaatgcgg tttatatttg taaattcggg 120
cacgcttgcg aaatggacat gtacatgcga cggaaatgcc aggagtgccg cctgaagaag 180
tgcttagctg taggcatg 198

<210> 42
<211> 66
<212> PRT
<213> Choristoneura fumiferana

<400> 42

Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu
1 5 10 15

Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr Lys Asn
20 25 30

Ala Val Tyr Ile Cys Lys Phe Gly His Ala Cys Glu Met Asp Met Tyr
35 40 45

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Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val
 50 55 60

Gly Met
 65

<210> 43
 <211> 441
 <212> DNA
 <213> Saccharomyces cerevisiae

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 43
 atgaagctac tgtcttctat cgaacaagca tgcgatattt gccgacttaa aaagctcaag 60
 tgctccaaag aaaaaccgaa gtgcgccaaag tgtctgaaga acaactggga gtgtcgctac 120
 tctcccaaaa ccaaaaggtc tccgctgact agggcacatc tgacagaagt ggaatcaagg 180
 ctagaaagac tggaacagct atttctactg atttttcctc gagaagacct tgacatgatt 240
 ttgaaaatgg attctttaca ggatataaaa gcattgttaa caggattatt tgtacaagat 300
 aatgtgaata aagatgccgt cacagataga ttggcttcag tggagactga tatgcctcta 360
 acattgagac agcatagaat aagtgcgaca tcatcatcgg aagagagtag taacaaaggt 420
 caaagacagt tgactgtatc g 441

<210> 44
 <211> 147
 <212> PRT
 <213> Saccharomyces cerevisiae

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 44

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu
 1 5 10 15

Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
 20 25 30

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Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

Phe Val Gln Asp Asn Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala
 100 105 110

Ser Val Glu Thr Asp Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser
 115 120 125

Ala Thr Ser Ser Ser Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu
 130 135 140

Thr Val Ser
 145

<210> 45
 <211> 606
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 45
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 aacgcggctg aagaacatct gaaggcgctg gcacgcaaag gcgttattga aattgtttcc 180
 ggcgcatacac gcgggattcg tctgttgcag gaagaggaag aagggttgcc gctggttagt 240
 cgtgtggctg ccggtgaacc acttctggcg caacagcata ttgaagggtca ttatcagggtc 300
 gatccttcct tattcaagcc gaatgctgat ttctgctgc gcgtcagcgg gatgtcgatg 360
 aaagatatcg gcattatgga tgggtgacttg ctggcagtgc ataaaactca ggatgtacgt 420

09955703-09501

aacggtcagg tcgttgtcgc acgtattgat gacgaagtta ccgttaagcg cctgaaaaaa 480
cagggcaata aagtcgaact gttgccagaa aatagcgagt ttaaaccaat tgcgtagat 540
cttcgtcagc agagcttcac cattgaaggg ctggcgggtg gggttattcg caacggcgac 600
tggtctg 606

<210> 46
<211> 202
<212> PRT
<213> Escherichia coli

<220>
<221> misc_feature
<223> Novel Sequence

<400> 46

Met Lys Ala Leu Thr Ala Arg Gln Gln Glu Val Phe Asp Leu Ile Arg
1 5 10 15

Asp His Ile Ser Gln Thr Gly Met Pro Pro Thr Arg Ala Glu Ile Ala
20 25 30

Gln Arg Leu Gly Phe Arg Ser Pro Asn Ala Ala Glu Glu His Leu Lys
35 40 45

Ala Leu Ala Arg Lys Gly Val Ile Glu Ile Val Ser Gly Ala Ser Arg
50 55 60

Gly Ile Arg Leu Leu Gln Glu Glu Glu Gly Leu Pro Leu Val Gly
65 70 75 80

Arg Val Ala Ala Gly Glu Pro Leu Leu Ala Gln Gln His Ile Glu Gly
85 90 95

His Tyr Gln Val Asp Pro Ser Leu Phe Lys Pro Asn Ala Asp Phe Leu
100 105 110

Leu Arg Val Ser Gly Met Ser Met Lys Asp Ile Gly Ile Met Asp Gly
115 120 125

Asp Leu Leu Ala Val His Lys Thr Gln Asp Val Arg Asn Gly Gln Val
130 135 140

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Val Val Ala Arg Ile Asp Asp Glu Val Thr Val Lys Arg Leu Lys Lys
145 150 155 160

Gln Gly Asn Lys Val Glu Leu Leu Pro Glu Asn Ser Glu Phe Lys Pro
165 170 175

Ile Val Val Asp Leu Arg Gln Gln Ser Phe Thr Ile Glu Gly Leu Ala
180 185 190

Val Gly Val Ile Arg Asn Gly Asp Trp Leu
195 200

<210> 47

<211> 420

<212> DNA

<213> Choristoneura fumiferana

<400> 47

atgagacgcc gctggtccaa caacgggggc ttccagacgc tgcgaatgct cgaggagagc 60

tcgtccgaag tgacgtcgtc ctcagctctg ggtctgccgg ccgcatggt tatgtctccg 120

gagtcgctcg cctcgccaga gtacggcggg ctcgagctct ggggatacga cgatggggtg 180

tcatacaaca cggcgcagtc cttgctgggc aatacttgca cgatgcagca gcagcaacag 240

acgcagccgc tgccgtcgat gccgttgct atgccgccga ccacgccgaa gtctgaaaac 300

gagtctattt cctcaggccg tgaggaactg tcgccagctt caagtataaa tgggtgcagt 360

acagatggcg aggcacgacg tcagaagaag ggccctgcmc cccgtcagca agaggaactg 420

<210> 48

<211> 140

<212> PRT

<213> Choristoneura fumiferana

<400> 48

Met Arg Arg Arg Trp Ser Asn Asn Gly Gly Phe Gln Thr Leu Arg Met
1 5 10 15

Leu Glu Glu Ser Ser Ser Glu Val Thr Ser Ser Ser Ala Leu Gly Leu
20 25 30

Pro Ala Ala Met Val Met Ser Pro Glu Ser Leu Ala Ser Pro Glu Tyr
35 40 45

Gly Gly Leu Glu Leu Trp Gly Tyr Asp Asp Gly Leu Ser Tyr Asn Thr

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50

55

60

Ala Gln Ser Leu Leu Gly Asn Thr Cys Thr Met Gln Gln Gln Gln Gln
65 70 75 80

Thr Gln Pro Leu Pro Ser Met Pro Leu Pro Met Pro Pro Thr Thr Pro
85 90 95

Lys Ser Glu Asn Glu Ser Ile Ser Ser Gly Arg Glu Glu Leu Ser Pro
100 105 110

Ala Ser Ser Ile Asn Gly Cys Ser Thr Asp Gly Glu Ala Arg Arg Gln
115 120 125

Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu Glu Leu
130 135 140

<210> 49
<211> 271
<212> DNA
<213> herpes simplex virus 7

<220>
<221> misc_feature
<223> Novel Sequence

<400> 49
atggggcccta aaaagaagcg taaagtcgcc ccccgaccg atgtcagcct gggggacgag 60
ctccacttag acggcgagga cgtggcgatg gcgcagccg acgcgctaga cgatttcgat 120
ctggacatgt tgggggacgg ggattccccg gggccgggat ttacccccca cgactccgcc 180
ccctacggcg ctctggatat ggccgacttc gagtttgagc agatgtttac cgatgccctt 240
ggaattgacg agtacggtgg ggaattcccg g 271

<210> 50
<211> 90
<212> PRT
<213> herpes simplex virus 7

<220>
<221> misc_feature
<223> Novel Sequence

<400> 50

09965703.059601

Met Gly Pro Lys Lys Lys Arg Lys Val Ala Pro Pro Thr Asp Val Ser
1 5 10 15

Leu Gly Asp Glu Leu His Leu Asp Gly Glu Asp Val Ala Met Ala His
20 25 30

Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Asp Gly Asp
35 40 45

Ser Pro Gly Pro Gly Phe Thr Pro His Asp Ser Ala Pro Tyr Gly Ala
50 55 60

Leu Asp Met Ala Asp Phe Glu Phe Glu Gln Met Phe Thr Asp Ala Leu
65 70 75 80

Gly Ile Asp Glu Tyr Gly Gly Glu Phe Pro
85 90

<210> 51
<211> 307
<212> DNA
<213> Saccharomyces cerevisiae

<400> 51
atgggtgctc ctccaaaaa gaagagaaag gtagctggta tcaataaaga tatcgaggag 60
tgcaatgcca tcattgagca gtttatcgac tacctgcgca ccggacagga gatgccgatg 120
gaaatggcgg atcaggcgat taacgtgggtg ccgggcatga cgccgaaaac cattcttcac 180
gccggggccgc cgatccagcc tgactggctg aaatcgaatg gttttcatga aattgaagcg 240
gatgttaacg ataccagcct ottgctgagt ggagatgcct cctaccctta tgatgtgcca 300
gattatg 307

<210> 52
<211> 102
<212> PRT
<213> Saccharomyces cerevisiae

<400> 52

Met Gly Ala Pro Pro Lys Lys Lys Arg Lys Val Ala Gly Ile Asn Lys
1 5 10 15

Asp Ile Glu Glu Cys Asn Ala Ile Ile Glu Gln Phe Ile Asp Tyr Leu
20 25 30

099570-09501

Arg Thr Gly Gln Glu Met Pro Met Glu Met Ala Asp Gln Ala Ile Asn
35 40 45

Val Val Pro Gly Met Thr Pro Lys Thr Ile Leu His Ala Gly Pro Pro
50 55 60

Ile Gln Pro Asp Trp Leu Lys Ser Asn Gly Phe His Glu Ile Glu Ala
65 70 75 80

Asp Val Asn Asp Thr Ser Leu Leu Leu Ser Gly Asp Ala Ser Tyr Pro
85 90 95

Tyr Asp Val Pro Asp Tyr
100

<210> 53
<211> 807
<212> DNA
<213> Homo sapiens

<400> 53
cccatggaat tccagtacct gccagatata gacgatcgtc accggattga ggagaaacgt 60
aaaaggacat atgagacctt caagagcatc atgaagaaga gtcctttcag cggacccacc 120
gacccccggc ctccacctcg acgcattgct gtgccttccc gcagctcagc ttctgtcccc 180
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ccacctgccc ccaagcccac ccaggctggg gaaggaacgc tgtcagaggc cctgctgcag 480
ctgcagtttg atgatgaaga cctggggggc ttgcttggca acagcacaga cccagctgtg 540
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cctgtggccc cccacacaac tgagcccatg ctgatggagt accctgaggc tataactcgc 660
ctagtgcag gggcccagag gccccccgac ccagctcctg ctccactggg ggccccgggg 720
ctccccaatg gcctcctttc aggagatgaa gacttctcct ccattgcgga catggacttc 780
tcagccctgc tgagtcagat cagctcc 807

<210> 54

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<211> 269
<212> PRT
<213> Homo sapiens

<400> 54

Pro Met Glu Phe Gln Tyr Leu Pro Asp Thr Asp Asp Arg His Arg Ile
1 5 10 15

Glu Glu Lys Arg Lys Arg Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys
20 25 30

Lys Ser Pro Phe Ser Gly Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg
35 40 45

Ile Ala Val Pro Ser Arg Ser Ser Ala Ser Val Pro Lys Pro Ala Pro
50 55 60

Gln Pro Tyr Pro Phe Thr Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu
65 70 75 80

Phe Pro Thr Met Val Phe Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala
85 90 95

Leu Ala Pro Ala Pro Pro Gln Val Leu Pro Gln Ala Pro Ala Pro Ala
100 105 110

Pro Ala Pro Ala Met Val Ser Ala Leu Ala Gln Ala Pro Ala Pro Val
115 120 125

Pro Val Leu Ala Pro Gly Pro Pro Gln Ala Val Ala Pro Pro Ala Pro
130 135 140

Lys Pro Thr Gln Ala Gly Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln
145 150 155 160

Leu Gln Phe Asp Asp Glu Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr
165 170 175

Asp Pro Ala Val Phe Thr Asp Leu Ala Ser Val Asp Asn Ser Glu Phe
180 185 190

Gln Gln Leu Leu Asn Gln Gly Ile Pro Val Ala Pro His Thr Thr Glu
195 200 205

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Pro Met Leu Met Glu Tyr Pro Glu Ala Ile Thr Arg Leu Val Thr Gly
 210 215 220

Ala Gln Arg Pro Pro Asp Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly
 225 230 235 240

Leu Pro Asn Gly Leu Leu Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala
 245 250 255

Asp Met Asp Phe Ser Ala Leu Leu Ser Gln Ile Ser Ser
 260 265

<210> 55
 <211> 225
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 55
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 gggttcaatgc acttgtccaa tgtcgagaga caaggggggtt caatgcactt gtccaatgtc 180
 gagagacaag ggggttcaat gcacttgtcc aatgtcgact ctaga 225

<210> 56
 <211> 19
 <212> DNA
 <213> Saccharomyces cerevisiae

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 56
 ggagtactgt cctccgagc 19

<210> 57
 <211> 666
 <212> DNA
 <213> Escherichia coli

<220>

0956703-095601

<221> misc_feature
<223> Novel Sequence

<400> 57
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ttagctctac cacagtgtgt gaaccaatgt atccagcacc acctgtaacc aaaacaattt 120
tagaagtact ttcactttgt aactgagctg tcatttataat tgaattttca aaaatttctta 180
cttttttttt ggatggacgc aaagaagttt aataatcata ttacatggca ttaccaccat 240
atacatatcc atatacatat ccataatctaa tcttacctcg actgctgtat ataaaaccag 300
tggttatatg tacagtactg ctgtatataa aaccagtggg tatatgtaca gtacgtcgac 360
tgctgtatat aaaaccagtg gttatatgta cagtactgct gtatataaaa ccagtgggta 420
tatgtacagt acgtcgaggg atgataatgc gattagtttt ttagccttat ttctggggta 480
attaatcagc gaagcgatga tttttgatct attaacagat atataaatgc aaaaactgca 540
taaccacttt aactaatact ttcaacattt tcggtttgta ttacttctta ttcaaatgta 600
ataaaagtat caacaaaaaa ttgttaatat acctctatac tttaacgtca aggagaaaaa 660
actata 666

<210> 58
<211> 1542
<212> DNA
<213> Choristoneura fumiferana

<220>
<221> misc_feature
<223> Novel Sequence

<400> 58
ctggacctga aacacgaagt ggcttaccga ggggtgctcc caggccaggt gaaggccgaa 60
ccgggggtcc acaacggcca ggtcaacggc cacgtgaggg actggatggc aggcggcgct 120
ggtgccaatt cgccgtctcc gggagcgggtg gctcaacccc agcctaacia tgggtattcg 180
tcgccactct cctcgggaag ctacggggcc tacagtccaa atgggaaaat aggccgtgag 240
gaactgtcgc cagcttcaag tataaatggg tgcagtacag atggcgaggc acgacgtcag 300
aagaagggcc ctgcgccccg tcagcaagag gaactgtgtc tggatgctgg ggacagagcc 360
tccggatacc actacaatgc gtcacgtgt gaagggtgta aagggttctt cagacggagt 420
gttacaaaa atgcggttta tatttgtaaa ttcggtcacg cttgcgaaat ggacatgtac 480

09965703.092601

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atgcgacgga aatgccagga gtgccgcctg aagaagtgct tagctgtagg catgaggcct 540
gagtgcgtag taccgcgagac tcagtgcgcc atgaagcgga aagagaagaa agcacagaag 600
gagaaggaca aactgcctgt cagcacgacg acggtggacg accacatgcc gccattatg 660
cagtgtgaac ctccacctcc tgaagcagca aggattcacg aagtgggtccc aaggtttctc 720
tccgacaagc tgttggagac aaaccggcag aaaaacatcc cccagttgac agccaaccag 780
cagttcctta tcgccaggct catctggtac caggacgggt acgagcagcc ttctgatgaa 840
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<210> 59
<211> 513
<212> PRT
<213> Choristoneura fumiferana

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<220>
<221> misc_feature
<223> Novel Sequence

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<400> 59

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Leu Asp Leu Lys His Glu Val Ala Tyr Arg Gly Val Leu Pro Gly Gln
1           5           10           15

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Val Lys Ala Glu Pro Gly Val His Asn Gly Gln Val Asn Gly His Val
          20           25           30

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Arg Asp Trp Met Ala Gly Gly Ala Gly Ala Asn Ser Pro Ser Pro Gly
35 40 45

Ala Val Ala Gln Pro Gln Pro Asn Asn Gly Tyr Ser Ser Pro Leu Ser
50 55 60

Ser Gly Ser Tyr Gly Pro Tyr Ser Pro Asn Gly Lys Ile Gly Arg Glu
65 70 75 80

Glu Leu Ser Pro Ala Ser Ser Ile Asn Gly Cys Ser Thr Asp Gly Glu
85 90 95

Ala Arg Arg Gln Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu Glu Leu
100 105 110

Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu
115 120 125

Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr Lys Asn
130 135 140

Ala Val Tyr Ile Cys Lys Phe Gly His Ala Cys Glu Met Asp Met Tyr
145 150 155 160

Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val
165 170 175

Gly Met Arg Pro Glu Cys Val Val Pro Glu Thr Gln Cys Ala Met Lys
180 185 190

Arg Lys Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Leu Pro Val Ser
195 200 205

Thr Thr Thr Val Asp Asp His Met Pro Pro Ile Met Gln Cys Glu Pro
210 215 220

Pro Pro Pro Glu Ala Ala Arg Ile His Glu Val Val Pro Arg Phe Leu
225 230 235 240

Ser Asp Lys Leu Leu Glu Thr Asn Arg Gln Lys Asn Ile Pro Gln Leu
245 250 255

Thr Ala Asn Gln Gln Phe Leu Ile Ala Arg Leu Ile Trp Tyr Gln Asp

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260

265

270

Gly Tyr Glu Gln Pro Ser Asp Glu Asp Leu Lys Arg Ile Thr Gln Thr
275 280 285

Trp Gln Gln Ala Asp Asp Glu Asn Glu Glu Ser Asp Thr Pro Phe Arg
290 295 300

Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe
305 310 315 320

Ala Lys Gly Leu Pro Gly Phe Ala Lys Ile Ser Gln Pro Asp Gln Ile
325 330 335

Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Val Ala
340 345 350

Arg Arg Tyr Asp Ala Ala Ser Asp Ser Val Leu Phe Ala Asn Asn Gln
355 360 365

Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ala Tyr Val Ile
370 375 380

Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Ala Leu Asp
385 390 395 400

Asn Ile His Tyr Ala Leu Leu Thr Ala Val Val Ile Phe Ser Asp Arg
405 410 415

Pro Gly Leu Glu Gln Pro Gln Leu Val Glu Glu Ile Gln Arg Tyr Tyr
420 425 430

Leu Asn Thr Leu Arg Ile Tyr Ile Leu Asn Gln Leu Ser Gly Ser Ala
435 440 445

Arg Ser Ser Val Ile Tyr Gly Lys Ile Leu Ser Ile Leu Ser Glu Leu
450 455 460

Arg Thr Leu Gly Met Gln Asn Ser Asn Met Cys Ile Ser Leu Lys Leu
465 470 475 480

Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp Val Ala
485 490 495

Asp Met Ser His Thr Gln Pro Pro Ile Leu Glu Ser Pro Thr Asn
500 505 510

Leu

<210> 60
<211> 4375
<212> DNA
<213> Choristoneura fumiferana

<220>
<221> misc_feature
<223> Novel Sequence

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<210> 61
 <211> 472
 <212> PRT

<213> Choristoneura fumiferana

<220>

<221> misc_feature

<223> Novel Sequence

<400> 61

Met Ser Ser Val Ala Lys Lys Asp Lys Pro Thr Met Ser Val Thr Ala
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Leu Ile Asn Trp Ala Arg Pro Ala Pro Pro Gly Pro Pro Gln Pro Gln
20 25 30

Ser Ala Ser Pro Ala Pro Ala Ala Met Leu Gln Gln Leu Pro Thr Gln
35 40 45

Ser Met Gln Ser Leu Asn His Ile Pro Thr Val Asp Cys Ser Leu Asp
50 55 60

Met Gln Trp Leu Asn Leu Glu Pro Gly Phe Met Ser Pro Met Ser Pro
65 70 75 80

Pro Glu Met Lys Pro Asp Thr Ala Met Leu Asp Gly Leu Arg Asp Asp
85 90 95

Ala Thr Ser Pro Pro Asn Phe Lys Asn Tyr Pro Pro Asn His Pro Leu
100 105 110

Ser Gly Ser Lys His Leu Cys Ser Ile Cys Gly Asp Arg Ala Ser Gly
115 120 125

Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys
130 135 140

Arg Thr Val Arg Lys Asp Leu Ser Tyr Ala Cys Arg Glu Glu Arg Asn
145 150 155 160

Cys Ile Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr
165 170 175

Gln Lys Cys Leu Ala Cys Gly Met Lys Arg Glu Ala Val Gln Glu Glu
180 185 190

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Arg Gln Arg Asn Ala Arg Gly Ala Glu Asp Ala His Pro Ser Ser Ser
195 200 205

Val Gln Val Ser Asp Glu Leu Ser Ile Glu Arg Leu Thr Glu Met Glu
210 215 220

Ser Leu Val Ala Asp Pro Ser Glu Glu Phe Gln Phe Leu Arg Val Gly
225 230 235 240

Pro Asp Ser Asn Val Pro Pro Arg Tyr Arg Ala Pro Val Ser Ser Leu
245 250 255

Cys Gln Ile Gly Asn Lys Gln Ile Ala Ala Leu Val Val Trp Ala Arg
260 265 270

Asp Ile Pro His Phe Gly Gln Leu Glu Leu Asp Asp Gln Val Val Leu
275 280 285

Ile Lys Ala Ser Trp Asn Glu Leu Leu Leu Phe Ala Ile Ala Trp Arg
290 295 300

Ser Met Glu Tyr Leu Glu Asp Glu Arg Glu Asn Gly Asp Gly Thr Arg
305 310 315 320

Ser Thr Thr Gln Pro Gln Leu Met Cys Leu Met Pro Gly Met Thr Leu
325 330 335

His Arg Asn Ser Ala Gln Gln Ala Gly Val Gly Ala Ile Phe Asp Arg
340 345 350

Val Leu Ser Glu Leu Ser Leu Lys Met Arg Thr Leu Arg Met Asp Gln
355 360 365

Ala Glu Tyr Val Ala Leu Lys Ala Ile Val Leu Leu Asn Pro Asp Val
370 375 380

Lys Gly Leu Lys Asn Arg Gln Glu Val Asp Val Leu Arg Glu Lys Met
385 390 395 400

Phe Ser Cys Leu Asp Asp Tyr Cys Arg Arg Ser Arg Ser Asn Glu Glu
405 410 415

Gly Arg Phe Ala Ser Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile

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420

425

430

Ser Leu Lys Ser Phe Glu His Leu Tyr Phe Phe His Leu Val Ala Glu
 435 440 445

Gly Ser Ile Ser Gly Tyr Ile Arg Glu Ala Leu Arg Asn His Ala Pro
 450 455 460

Pro Ile Asp Val Asn Ala Met Met
 465 470

<210> 62

<211> 1404

<212> DNA

<213> Mus musculus

<220>

<221> misc_feature

<223> Novel Sequence

<400> 62

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 ggaatcggct ctccactggg ctgcctggg cagctgcact ctctatcag caccctgagc 180
 tccccatca atggcatggg tccgcccttc tctgtcatca gctcccccat gggcccgac 240
 tccatgtcgg taccaccac accacattg ggcttcggga ctggtagccc ccagctcaat 300
 tcacccatga accctgtgag cagcactgag gatatcaagc cgccactagg cctcaatggc 360
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 gctatctgtg gggaccgctc ctccaggcaa cactatgggg tatacagttg tgagggctgc 480
 aagggcttct tcaagaggac agtacgcaa gacctgacct acacctgccg agacaacaag 540
 gactgcctga tcgacaagag acagcggaac cgggtgtcagt actgccgcta ccagaagtgc 600
 ctggccatgg gcatgaagcg ggaagctgtg caggaggagc ggcagcgggg caaggaccgg 660
 aatgagaacg aggtggagtc caccagcagt gccaacgagg acatgcctgt agagaagatt 720
 ctggaagccg agcttgctgt cgagcccaag actgagacat acgtggaggc aaacatgggg 780
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 gaccaggtca tctgtctacg ggcaggctgg aacgagctgc tgatcgctc cttctccac 960

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<210> 63
 <211> 467
 <212> PRT
 <213> Mus musculus
 <220>
 <221> misc_feature
 <223> Novel Sequence

<400> 63

Met Asp Thr Lys His Phe Leu Pro Leu Asp Phe Ser Thr Gln Val Asn
 1 5 10 15

Ser Ser Ser Leu Asn Ser Pro Thr Gly Arg Gly Ser Met Ala Val Pro
 20 25 30

Ser Leu His Pro Ser Leu Gly Pro Gly Ile Gly Ser Pro Leu Gly Ser
 35 40 45

Pro Gly Gln Leu His Ser Pro Ile Ser Thr Leu Ser Ser Pro Ile Asn
 50 55 60

Gly Met Gly Pro Pro Phe Ser Val Ile Ser Ser Pro Met Gly Pro His
 65 70 75 80

Ser Met Ser Val Pro Thr Thr Pro Thr Leu Gly Phe Gly Thr Gly Ser
 85 90 95

Pro Gln Leu Asn Ser Pro Met Asn Pro Val Ser Ser Thr Glu Asp Ile
 100 105 110

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Lys Pro Pro Leu Gly Leu Asn Gly Val Leu Lys Val Pro Ala His Pro
 115 120 125

Ser Gly Asn Met Ala Ser Phe Thr Lys His Ile Cys Ala Ile Cys Gly
 130 135 140

Asp Arg Ser Ser Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys
 145 150 155 160

Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asp Leu Thr Tyr Thr Cys
 165 170 175

Arg Asp Asn Lys Asp Cys Leu Ile Asp Lys Arg Gln Arg Asn Arg Cys
 180 185 190

Gln Tyr Cys Arg Tyr Gln Lys Cys Leu Ala Met Gly Met Lys Arg Glu
 195 200 205

Ala Val Gln Glu Glu Arg Gln Arg Gly Lys Asp Arg Asn Glu Asn Glu
 210 215 220

Val Glu Ser Thr Ser Ser Ala Asn Glu Asp Met Pro Val Glu Lys Ile
 225 230 235 240

Leu Glu Ala Glu Leu Ala Val Glu Pro Lys Thr Glu Thr Tyr Val Glu
 245 250 255

Ala Asn Met Gly Leu Asn Pro Ser Ser Pro Asn Asp Pro Val Thr Asn
 260 265 270

Ile Cys Gln Ala Ala Asp Lys Gln Leu Phe Thr Leu Val Glu Trp Ala
 275 280 285

Lys Arg Ile Pro His Phe Ser Glu Leu Pro Leu Asp Asp Gln Val Ile
 290 295 300

Leu Leu Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His
 305 310 315 320

Arg Ser Ile Ala Val Lys Asp Gly Ile Leu Leu Ala Thr Gly Leu His
 325 330 335

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Val His Arg Asn Ser Ala His Ser Ala Gly Val Gly Ala Ile Phe Asp
 340 345 350

Arg Val Leu Thr Glu Leu Val Ser Lys Met Arg Asp Met Gln Met Asp
 355 360 365

Lys Thr Glu Leu Gly Cys Leu Arg Ala Ile Val Leu Phe Asn Pro Asp
 370 375 380

Ser Lys Gly Leu Ser Asn Pro Ala Glu Val Glu Ala Leu Arg Glu Lys
 385 390 395 400

Val Tyr Ala Ser Leu Glu Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln
 405 410 415

Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser
 420 425 430

Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe Phe Lys Leu Ile Gly
 435 440 445

Asp Thr Pro Ile Asp Thr Phe Leu Met Glu Met Leu Glu Ala Pro His
 450 455 460

Gln Ala Thr
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<210> 64
 <211> 309
 <212> DNA
 <213> Simian virus 40

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 64
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 ctccgcccag ttccgcccata tctccgcccc atggctgact aatttttttt atttatgcag 240
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gcctaggct

309

<210> 65
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic E1b minimal promoter

<220>
<221> misc_feature
<223> Novel Sequence

<400> 65
tatataatgg atccccgggt accg

24

<210> 66
<211> 1653
<212> DNA
<213> Photinus pyralis

<220>
<221> misc_feature
<223> Novel Sequence

<400> 66
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accgctggag agcaactgca taaggctatg aagagatacg ccctgggtcc tggaacaatt 120
gcttttacag atgcacatat cgagggtgaac atcacgtacg cggaatactt cgaaatgtcc 180
gttcggttgg cagaagctat gaaacgatat gggctgaata caaatcacag aatcgtcgta 240
tgcagtgaaa actctcttca attctttatg ccggtggttg gcgcgttatt tatcggagtt 300
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catgccagag atcctatttt tggcaatcaa atcattccgg atactgcat ttttaagtgtt 720
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 aaggccaaga agggcggaag gtccaaattg taa 1653

<210> 67
 <211> 867
 <212> DNA
 <213> Choristoneura fumiferana

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 67
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 tctttggtgg cagatcccag cgaggagtgc cagttctctc gcgtggggcc tgacagcaac 180
 gtgcctccac gttaccgcgc gcccgctctc tccctctgcc aaataggcaa caagcaaata 240
 gcggcggttg tggatggggc gcgcgacatc cctcatttcg ggcagctgga gctggacgat 300
 caagtggtag tcatcaaggc ctcttggaat gagctgctac tcttcgcat cgctggcg 360
 tctatggagt atttggaaga tgagagggag aacggggacg gaacgcggag caccactcag 420
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 cggctgccag ctctccgctc catctcgctc aagagcttcg aacacctcta cttcttccac 780
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<210> 68
 <211> 619
 <212> DNA
 <213> Cytomegalovirus

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 68
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 atgggtggag tatttacggt aaactgccc cttggcagta catcaagtgt atcatatgcc 180
 aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt atgcccagta 240
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 acggtgggag gtctatataa gcagagctcg tttagtgaac cgtcagatcg cctggagacg 540
 ccatccacgc tgttttgacc tccatagaag acaccgggac cgatccagcc tccgcgcccg 600
 ggaacggtgc attggaacg 619

<210> 69
 <211> 262
 <212> DNA
 <213> Rous sarcoma virus

<220>
 <221> misc_feature

<223> Novel Sequence

<400> 69

atgtagtctt atgcaatact cttgtagtct tgcaacatgg taacgatgag ttagcaacat 60
gccttacaag gagagaaaaa gcaccgtgca tgccgatagg tggaagtaag gtggtacgat 120
cgtgccttat taggaaggca acagacgggt ctgacatgga ttggacgaac cactgaattc 180
cgcatcgag agatattgta ttttaagtgcc tagctcgata caataaacgc catttgacca 240
ttcaccacat tggagtgcac ct 262

<210> 70

<211> 1247

<212> DNA

<213> *Choristoneura fumiferana*

<220>

<221> misc_feature

<223> Novel Sequence

<400> 70

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ctggtatgcg gggacagagc ctccggatag cactacaatg cgctcacgtg tgaaggggtgt 180
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gcttgcaaaa tggacatgta catgacgagc aaatgccagg agtgccgcct gaagaagtgc 300
ttagctgtag gcatgaggcc tgagtgcgta gtacccgaga ctacgtgcgc catgaagcgg 360
aaagagaaga aagcacagaa ggagaaggac aaactgcctg tcagcacgac gacgggtggac 420
gaccacatgc cgccattat gcagtgtgaa cctccacctc ctgaagcagc aaggattcac 480
gaagtgggtcc caaggtttct ctccgacaag ctggttgaga caaaccggca gaaaaacatc 540
ccccagttga cagccaacca gcagttcctt atcgccaggc tcatctggta ccaggacggg 600
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atgtgcatct ccctcaagct caagaacaga aagctgccgc ctttcct 1247

<210> 71
<211> 440
<212> PRT
<213> Choristoneura fumiferana

<220>
<221> misc_feature
<223> Novel Sequence

<400> 71

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Gly Cys Ser Thr Asp Gly Glu Ala Arg Arg Gln Lys Lys Gly Pro Ala
20 25 30

Pro Arg Gln Gln Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser
35 40 45

Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe
50 55 60

Arg Arg Ser Val Thr Lys Asn Ala Val Tyr Ile Cys Lys Phe Gly His
65 70 75 80

Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg
85 90 95

Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro
100 105 110

Glu Thr Gln Cys Ala Met Lys Arg Lys Glu Lys Lys Ala Gln Lys Glu
115 120 125

Lys Asp Lys Leu Pro Val Ser Thr Thr Thr Val Asp Asp His Met Pro

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130	135	140
Pro Ile Met Gln Cys Glu 145	Pro Pro Pro Pro 150	Glu Ala Ala Arg Ile His 155 160
Glu Val Val Pro Arg Phe Leu Ser Asp Lys Leu Leu Glu Thr Asn Arg 165		170 175
Gln Lys Asn Ile Pro Gln Leu Thr Ala Asn Gln Gln Phe Leu Ile Ala 180		185 190
Arg Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Asp Glu Asp 195		200 205
Leu Lys Arg Ile Thr Gln Thr Trp Gln Gln Ala Asp Asp Glu Asn Glu 210		215 220
Glu Ser Asp Thr Pro Phe Arg Gln Ile Thr Glu Met Thr Ile Leu Thr 225		230 235 240
Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Gly Phe Ala Lys 245		250 255
Ile Ser Gln Pro Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu 260		265 270
Val Met Met Leu Arg Val Ala Arg Arg Tyr Asp Ala Ala Ser Asp Ser 275		280 285
Val Leu Phe Ala Asn Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys 290		295 300
Ala Gly Met Ala Tyr Val Ile Glu Asp Leu Leu His Phe Cys Arg Cys 305		310 315 320
Met Tyr Ser Met Ala Leu Asp Asn Ile His Tyr Ala Leu Leu Thr Ala 325		330 335
Val Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Gln Pro Gln Leu Val 340		345 350
Glu Glu Ile Gln Arg Tyr Tyr Leu Asn Thr Leu Arg Ile Tyr Ile Leu 355		360 365

Asn Gln Leu Ser Gly Ser Ala Arg Ser Ser Val Ile Tyr Gly Lys Ile
 370 375 380

Leu Ser Ile Leu Ser Glu Leu Arg Thr Leu Gly Met Gln Asn Ser Asn
 385 390 395 400

Met Cys Ile Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu
 405 410 415

Glu Glu Ile Trp Asp Val Ala Asp Met Ser His Thr Gln Pro Pro Pro
 420 425 430

Ile Leu Glu Ser Pro Thr Asn Leu
 435 440

<210> 72
 <211> 943
 <212> DNA
 <213> Renilla

<220>
 <221> misc_feature
 <223> Novel Sequence

<400> 72
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 aaacatgcag aaaatgctgt taaaaaaaa catggtaacg cggcctcttc ttatttatgg 180
 cgacatgttg tgccacatat tgagccagta ggcgggtgta ttataccaga cttatttggt 240
 atgggcaa atcaggcaa atcggta atgggt tcttataggt tacttgatca ttacaaat at 300
 ctactgcat ggtttgaact tcttaattta ccaaagaaga tcatttttgt cggccatgat 360
 tggggtgctt gtttggcatt tcattatagc tatgagcatc aagataagat caaagcaata 420
 gttcacgctg aaagtgtagt agatgtgatt gaatcatggg atgaatggcc tgatattgaa 480
 gaagatattg cgttgatcaa atctgaagaa ggagaaaaaa tggttttgga gaataacttc 540
 ttcgtggaaa ccatgttgcc atcaaaaatc atgagaaagt tagaaccaga agaatttgca 600
 gcatatcttg aaccattcaa agagaaagggt gaagtctgct gtccaacatt atcatggcct 660
 cgtgaaatcc cgttagtaaa aggtggtaaa cctgacgttg taaaattgt taggaattat 720

0995703-092601

aatgcttatc tacgtgcaag tgatgattta ccaaaaatgt ttattgaatc ggacccagga 780
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 gtaaaagggtc ttcatTTTTc gcaagaagat gcacctgatg aaatgggaaa atatatcaaa 900
 tcgttcgttg agcgagttct caaaaatgaa caataattct aga 943

<210> 73
 <211> 530
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 73
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 aagactctcc tccgtgcgtc ctogtcttca ccggtcgcgt tcctgaaacg cagatgtgcc 180
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 aggaaaaatt ggcagtaacc tggccccaca aaccttcaaa tgaacgaatc aaattaacaa 300
 ccataggatg ataatgcgat tagtttttta gccttatttc tggggtaatt aatcagcgaa 360
 gcgatgattt ttgatctatt aacagatata taaatgcaaa aactgcataa ccactttaac 420
 taatactttc aacatTTTcg gtttgtatta cttcttattc aaatgtaata aaagtatcaa 480
 caaaaaattg ttaatatacc tctatacttt aacgtcaagg aggaattaag 530

<210> 74
 <211> 3157
 <212> DNA
 <213> *Escherichia coli*

<400> 74
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 cccgtcgttt tacaacgtcg tgactgggaa aaccctggcg ttaccaact taatcgctt 180
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 aatgttgatg aaagctggct acaggaaggc cagacgcgaa ttatttttga tggcgtaaac 540

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<210> 75
 <211> 185
 <212> DNA
 <213> Escherichia coli

<400> 75	
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aaccagtgggt tatatgtaca gtactgctgt atataaaacc agtgggtata tgtacagtac	180
gtcga	185